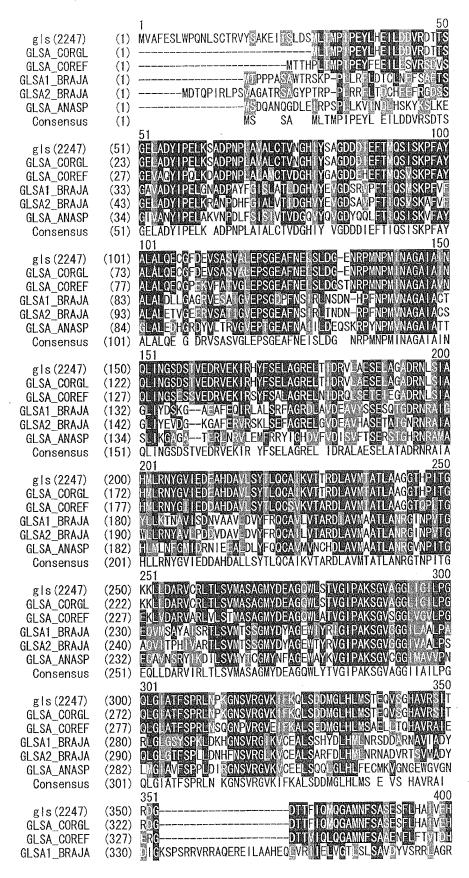
## EXHIBIT A

## Alignment of amino acid sequences of glutaminases



GLSA2_BRAJA		VYGISSRRSROPHEQQILDERHSDIR ELVEANGTI VYVTRR TSE
GLSA_ANASP Consensus		DDG DTTIIQLQGAMNFSASE FL   EH
gls (2247) GLSA_CORGL GLSA_COREF GLSA1_BRAJA GLSA2_BRAJA GLSA_ANASP	(379) (351) (356) (380) (390) (335)	450 NEGTEVVLDLTRVLSEHPVAIRMIKEGLKRIRDAGE VEILDPDDVLPD NEGTEVVLDLTRVLSEHPVAIRMIKEGLKRIRDAGE VEILDPDDVLPD DETGEKVVLDLSRVPMERPLGRRLVKEGLRRIRDNGEKVALYDPEDLPD P-RPGFVIEDLHRVTSTTRAGARLVAEAFEELAALNVTVV SGVRRASKE PPNAPLLIDFRRVPDITAAGAEL GETLTALGNANVTTILSGLEFASAV
Consensus	(401)	F G VVLDLTRV SF PVG RLIKEGLKRIRDAGF V I DPDDVLPD 451 500
gls (2247) GLSA_CORGL GLSA_COREF GLSA1_BRAJA GLSA2_BRAJA GLSA_ANASP	(429) (401) (406) (429) (440) (335)	MSDGI I CKERV————————————————————————————————————
Consensus	(451)	F FSDGT R 501 550
gls (2247) GLSA_CORGL GLSA_COREF GLSA1_BRAJA	(442) (414) (424) (479)	PLLEGLSADELAELGAICTIRTYQSGAKILTTGDPADALFFLRSGAVHVT
GLSA2_BRAJA GLSA_ANASP Consensus	(490) (335) (501)	ALLAELDTDE I AA I VKLSTTRHYTAGQRV I AAGAPANSLFFLQSGMVSVK
gls(2247) GLSA_CORGL	(442) (414)	551 600
GLSA_COREF GLSA1_BRAJA GLSA2_BRAJA GLSA_ANASP	(424) (529) (540) (335)	LPDGVRLATLTAGMAFGEMALLEQTRSADVFADMAATAFEAPLKDFERFR LRSGVRLASLGPGMEFGEMAILERTRSADVFADTPVACLELPLDSFADYR
Consensus	(551)	601 635
gls (2247) GLSA_CORGL GLSA_COREF	(442) (414) (424)	
GLSA1_BRAJA GLSA2_BRAJA GLSA_ANASP Consensus	(579) (590) (335) (601)	EQHPRASERIMRNLAQLLADRLIVANAKVDILTST RLHPETALKIMRNLAAILARRLVAANAKVDLLSAY
GLSA_COREF: GLSA1_BRAJA GLSA2_BRAJA	Q8FMX4 : Q89NA : Q89KV2	Corynebacterium glutamicum Corynebacterium efficiens. 7: Bradyrhizobium japonicum, 2: Bradyrhizobium japonicum Anabaena sp. (strain PCC 7120)